

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Hillman, Jennifer L.
Shah, Purvi
Murry, Lynn E.
- (ii) TITLE OF THE INVENTION: HUMAN LYSOPHOSPHOLIPASE
- (iii) NUMBER OF SEQUENCES: 3
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
 - (B) STREET: 3174 Porter Drive
 - (C) CITY: Palo Alto
 - (D) STATE: CA
 - (E) COUNTRY: USA
 - (F) ZIP: 94304
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette
 - (B) COMPUTER: IBM Compatible
 - (C) OPERATING SYSTEM: DOS
 - (D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: To Be Assigned
 - (B) FILING DATE: Filed Herewith
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Billings, Lucy J.
 - (B) REGISTRATION NUMBER: 36,749
 - (C) REFERENCE/DOCKET NUMBER: PF-0269 US
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 415-855-0555
 - (B) TELEFAX: 415-845-4166

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 208 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: KIDNNOT19
 - (B) CLONE: 2676650
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met	Cys	Gly	Asn	Asn	Met	Ser	Thr	Pro	Leu	Pro	Ala	Ile	Val	Pro	Ala
1				5				10					15		
Ala	Arg	Lys	Ala	Thr	Ala	Ala	Val	Ile	Phe	Leu	His	Gly	Leu	Gly	Asp
		20					25					30			
Thr	Gly	Pro	Val	Arg	Pro	Val	Thr	Leu	Asn	Met	Asn	Val	Ala	Met	Pro
		35				40						45			

Ser	Trp	Phe	Asp	Ile	Ile	Gly	Leu	Ser	Pro	Asp	Ser	Gln	Glu	Asp	Glu
50						55					60				
Ser	Gly	Ile	Lys	Gln	Ala	Glu	Asn	Ile	Lys	Ala	Leu	Ile	Asp	Gln	
65				70					75					80	
Glu	Val	Lys	Asn	Gly	Ile	Pro	Ser	Asn	Arg	Ile	Ile	Leu	Gly	Gly	Phe
			85					90					95		
Ser	Gln	Gly	Gly	Ala	Leu	Ser	Leu	Tyr	Thr	Ala	Leu	Thr	Thr	Gln	Gln
		100						105				110			
Lys	Leu	Ala	Gly	Val	Thr	Ala	Leu	Ser	Phe	Leu	Leu	Pro	Leu	Arg	Xaa
	115						120					125			
Ser	Phe	Pro	Gln	Gly	Pro	Ile	Gly	Gly	Ala	Asn	Arg	Asp	Ile	Ser	Ile
130						135					140				
Leu	Gln	Cys	His	Gly	Asp	Cys	Asp	Pro	Leu	Val	Pro	Leu	Met	Phe	Gly
145				150						155					160
Ser	Leu	Thr	Val	Glu	Lys	Leu	Lys	Thr	Leu	Val	Asn	Pro	Ala	Asn	Val
			165						170					175	
Thr	Phe	Lys	Thr	Tyr	Glu	Gly	Met	Met	His	Ser	Ser	Cys	Gln	Gln	Glu
		180						185					190		
Met	Met	Asp	Val	Lys	Gln	Phe	Ile	Asp	Lys	Leu	Leu	Pro	Pro	Ile	Asp
		195					200					205			

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 709 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: KIDNNOT19
- (B) CLONE: 2676650

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GCCGCTCGCA	CGCCCTTGGG	CCGCGGCCGG	GCGCCCGCTC	TTCCTTCCGC	TTGCGCTGTG	60
AGCTGAGGCG	GTGTATGTGC	GGCAATAACA	TGTCAACCCC	GCTGCCCGCC	ATCGTGCCCG	120
CCGCCCCGAA	GGCCACCGCT	GCGGTGATTT	TCCTGCATGG	ATTGGGAGAT	ACTGGGCCCTG	180
TTAGGCCTGT	TACATTAAAT	ATGAACGTGG	CTATGCCTTC	ATGGTTTGAT	ATTATTGGGC	240
TTTCACCAGA	TTCACAGGAG	GATGAATCTG	GGATTAAACA	GGCAGCAGAA	AATATAAAAG	300
CTTTGATTGA	TCAAGAAGTG	AAGAATGGCA	TTCCTTCTAA	CAGAATTATT	TTGGGAGGGT	360
TTTCTCAGGG	AGGAGCTTTA	TCTTTATATA	CTGCCCTTAC	CACACAGCAG	AAACTGGCAG	420
GTGTCACTGC	ACTCAGTTTC	TTGCTTCCAC	TTCGGGNTTC	CTTCCACAG	GGKCCTATCG	480
GTGGTGCTAA	TAGAGATATT	TCTATTCTCC	AGTGCCACGG	GGATTGTGAC	CCTTTGGTTC	540
CCCTGATGTT	TGGTCTCTCT	ACGGTGGAAA	AACTAAAAAC	ATTGGTGAAT	CCAGCCAATG	600
TGACCTTTAA	AACCTATGAA	GGTATGATGC	ACAGTTCGTG	TCAACAGGAA	ATGATGGATG	660
TCAAGCAATT	CATTGATAAA	CTCCTACCTC	CAATTGATTG	ACGTCACTA		709

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 230 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 1552244

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met	Cys	Gly	Asn	Asn	Met	Ser	Ala	Pro	Met	Pro	Ala	Val	Val	Pro	Ala	1	5	10	15
Ala	Arg	Lys	Ala	Thr	Ala	Ala	Val	Ile	Phe	Leu	His	Gly	Leu	Gly	Asp	20	25	30	
Thr	Gly	His	Gly	Trp	Ala	Glu	Ala	Phe	Ala	Gly	Ile	Lys	Ser	Ser	His	35	40	45	
Ile	Lys	Tyr	Ile	Cys	Pro	His	Ala	Pro	Val	Met	Pro	Val	Thr	Leu	Asn	50	55	60	
Met	Ser	Met	Met	Met	Pro	Ser	Trp	Phe	Asp	Ile	Ile	Gly	Leu	Ser	Pro	65	70	75	80
Asp	Ser	Gln	Glu	Asp	Glu	Ser	Gly	Ile	Lys	Gln	Ala	Ala	Glu	Thr	Val	85	90	95	
Lys	Ala	Leu	Ile	Asp	Gln	Glu	Val	Lys	Asn	Gly	Ile	Pro	Ser	Asn	Arg	100	105	110	
Ile	Ile	Leu	Gly	Gly	Phe	Ser	Gln	Gly	Gly	Ala	Leu	Ser	Leu	Tyr	Thr	115	120	125	
Ala	Leu	Thr	Thr	Gln	Gln	Lys	Leu	Ala	Gly	Val	Thr	Ala	Leu	Ser	Cys	130	135	140	
Trp	Leu	Pro	Leu	Arg	Ala	Ser	Phe	Ser	Gln	Gly	Pro	Ile	Asn	Ser	Ala	145	150	155	160
Asn	Arg	Asp	Ile	Ser	Val	Leu	Gln	Cys	His	Gly	Asp	Cys	Asp	Pro	Leu	165	170	175	
Val	Pro	Leu	Met	Phe	Gly	Ser	Leu	Thr	Val	Glu	Arg	Leu	Lys	Gly	Leu	180	185	190	
Val	Asn	Pro	Ala	Asn	Val	Thr	Phe	Lys	Val	Tyr	Glu	Gly	Met	Met	His	195	200	205	
Ser	Ser	Cys	Gln	Gln	Glu	Met	Met	Asp	Val	Lys	Tyr	Phe	Ile	Asp	Lys	210	215	220	
Leu	Leu	Pro	Pro	Ile	Asp											225	230		